BRAIN TUMOR SEGMENTATION

Under the Guidance of: Prof. Disha Wankhede

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INTRODUCTION

Brain tumor segmentation is a crucial task in medical image analysis, primarily aimed at identifying and delineating tumor regions within brain images obtained from various medical imaging modalities such as MRI (Magnetic Resonance Imaging) and CT (Computed Tomography) scans. Accurate segmentation of brain tumors is essential for diagnosis, treatment planning, and monitoring of patients with brain-related conditions. Machine learning techniques, particularly deep learning algorithms, have shown promising results in automating this segmentation process.

Project Overview

- Implementation of state-of-the-art machine learning models for brain tumor segmentation.
- Exploration of various neural network architectures, including convolutional neural networks (CNNs), for feature extraction and segmentation.We used resnet CNN Architecture in project.
- Integration of preprocessing techniques to enhance the quality of input brain images and improve the performance of the segmentation model.
- Evaluation of the developed models using standard metrics such as Dice Similarity Coefficient (DSC), sensitivity, specificity, and accuracy.
- Comparison of the proposed approach with existing methods and benchmarks to assess its effectiveness and performance.

DATASET

Dataset used in this project was provided by Kaggle Website.The name of dataset is Semantic Segmentation. This dataset contains 1502 T1-weighted contrast-enhanced images with three kinds of brain tumor. For a detailed information about the dataset please refer to following site:- https://www.kaggle.com/datasets/pkdarabi/brain-tumor-image-dataset-semantic-segmentation

Version 5 of this dataset is used in this project. Each image is of dimension 512 x 512 x 1 , these are black and white images thus having a single channel.
There are 420 Valid set images and 219 are test set Images .

Data Augmentation

The basic forms of data augmentation are used here to diversify the training data.

All the augmentation methods are used from Pytorch's Torchvision module.

- Horizontally Flip
- Vertically Flip
- Rotation Between 75°-15°

Code Responsible for augmentation:-

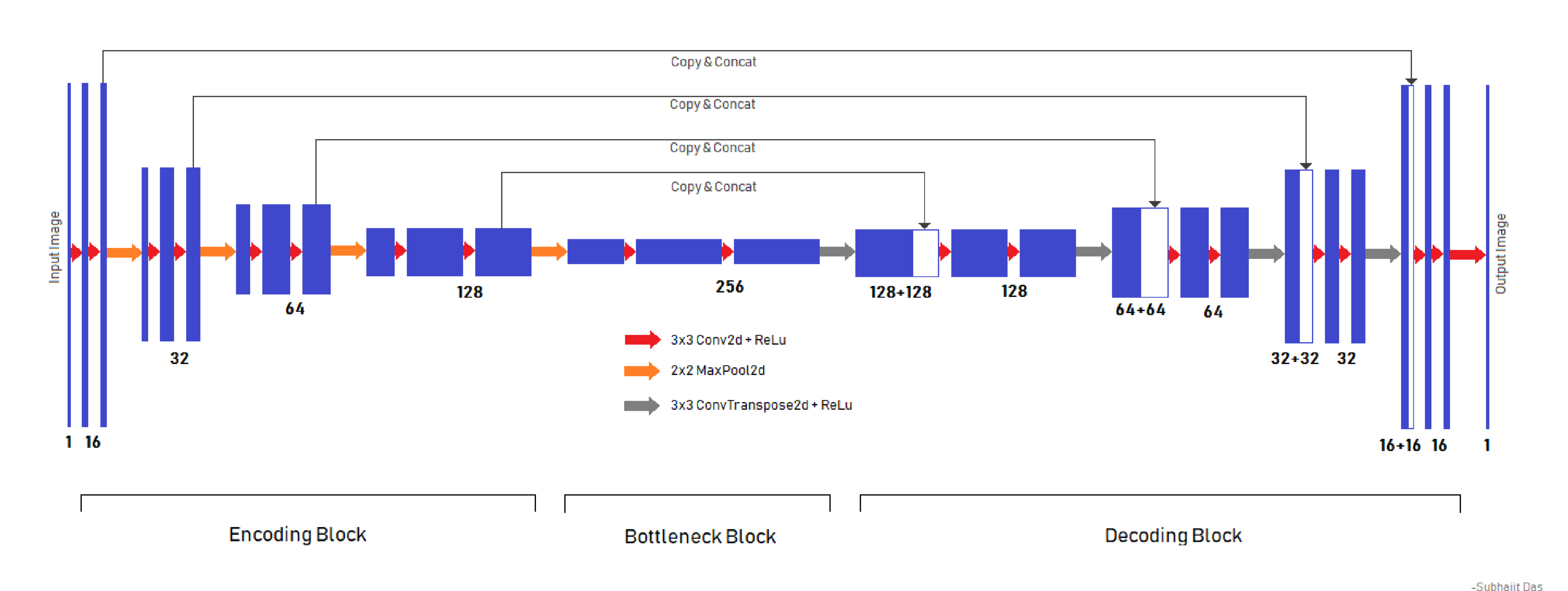
```
def _random_transform(self, image, mask):
        """ Applies a set of transformation in random order.
        Each transformation has a probability of 0.5
        """
        choice_list = list(self.transform)
        for _ in range(len(choice_list)):
            choice_key = random.choice(choice_list)
            action_prob = random.randint(0, 1)
            if action_prob >= 0.5:
                if choice_key == 'rotate':
                    rotation = random.randint(15, 75)
                    image = self.transform[choice_key](image, rotation)
                    mask = self.transform[choice_key](mask, rotation)
                else:
                    image = self.transform[choice_key](image)
                    mask = self.transform[choice_key](mask)
            choice_list.remove(choice_key)

        return image, mask
```

Model Architecture

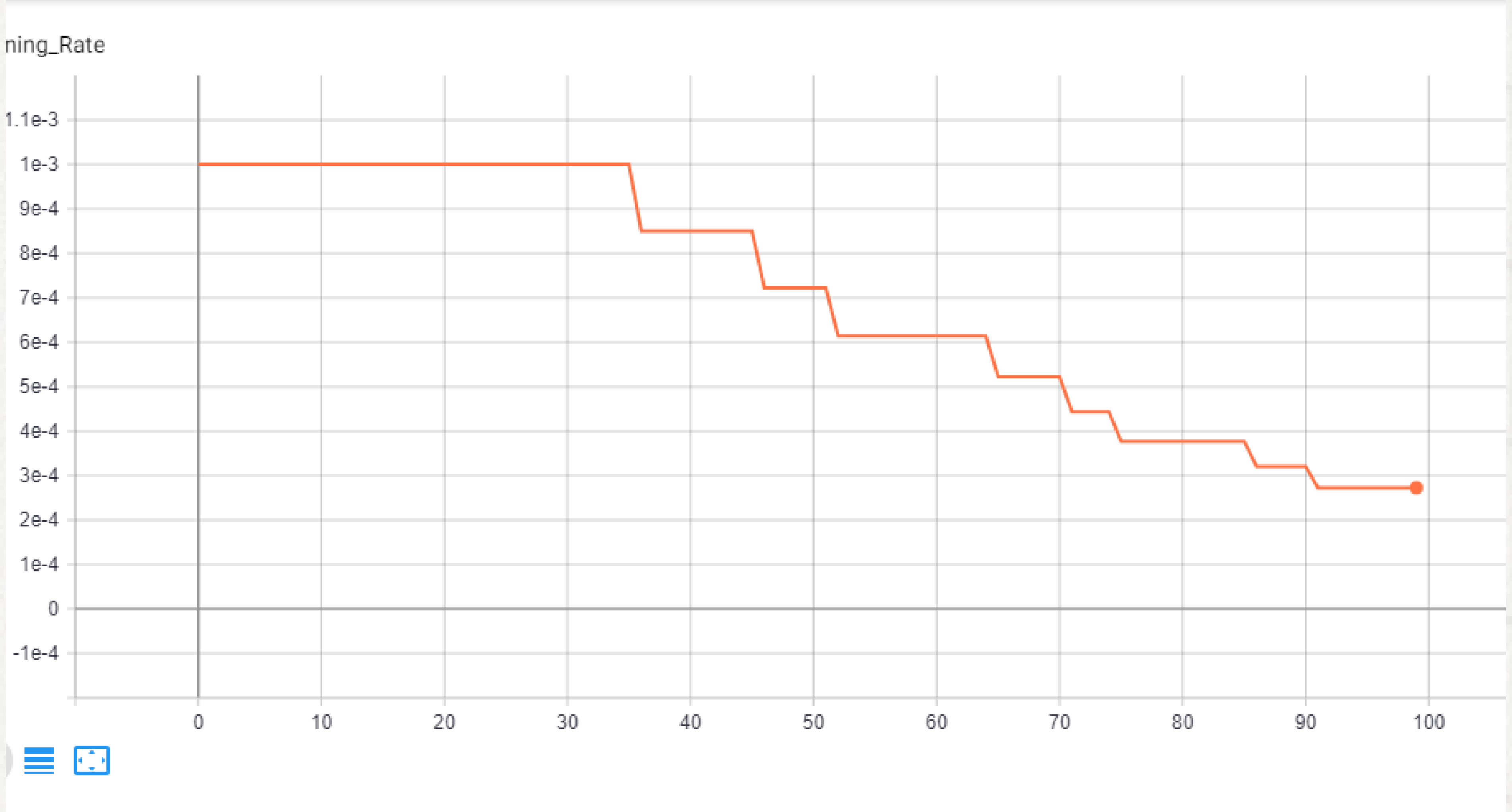
The feature extraction backbone consists of several convolutional layers, responsible for learning hierarchical features from the input MRI volumes. Common architectures used as feature extractors include:

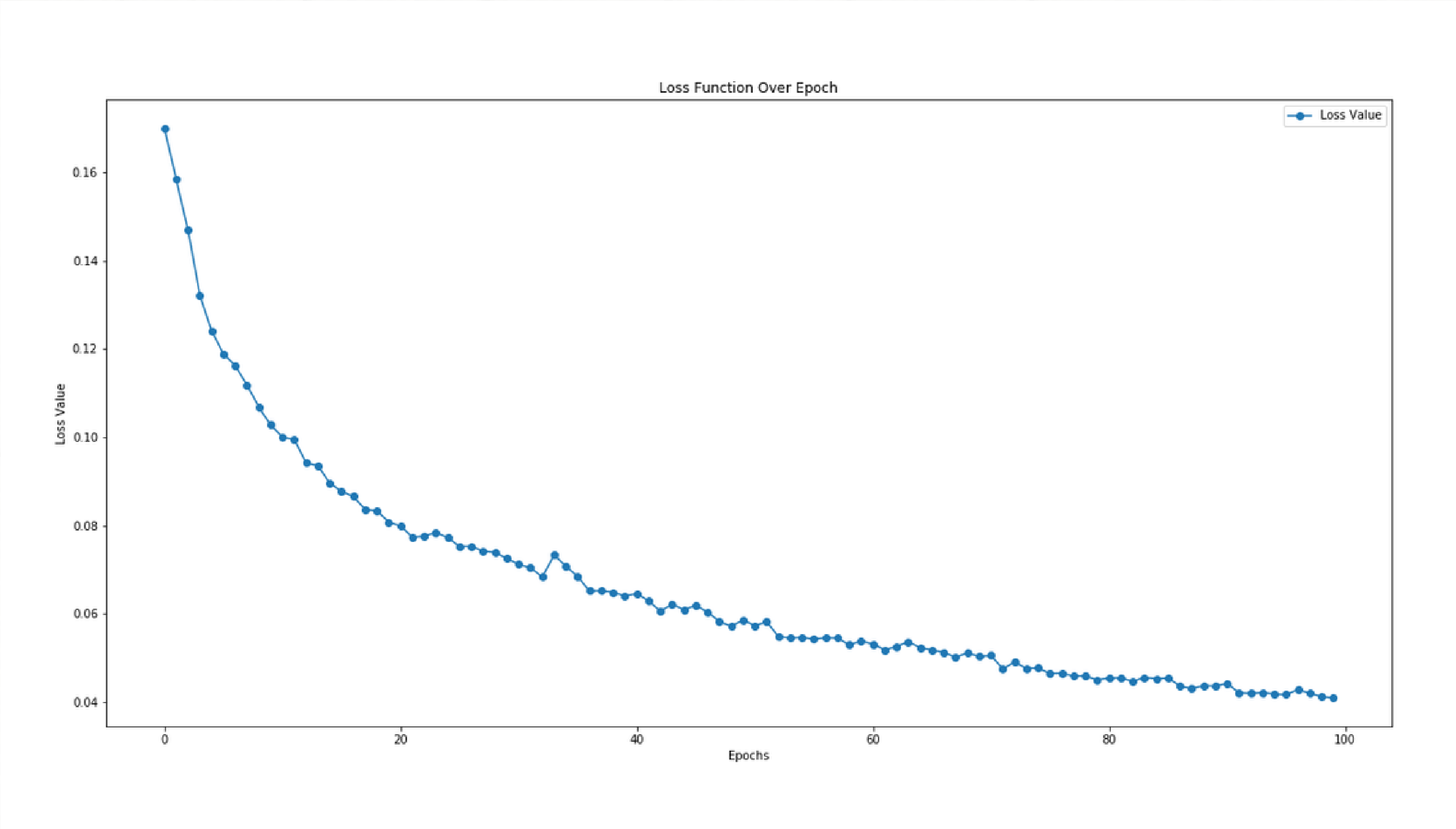
- U-Net: A popular architecture for biomedical image segmentation, comprising encoder and decoder pathways connected by skip connections to preserve spatial information.
- DeepLabv3: Utilizes atrous convolution and dilated convolutions to capture multi-scale contextual information and achieve precise segmentation boundaries.
- V-Net: Specifically designed for volumetric medical image segmentation, employing 3D convolutions and skip connections for efficient feature learning.



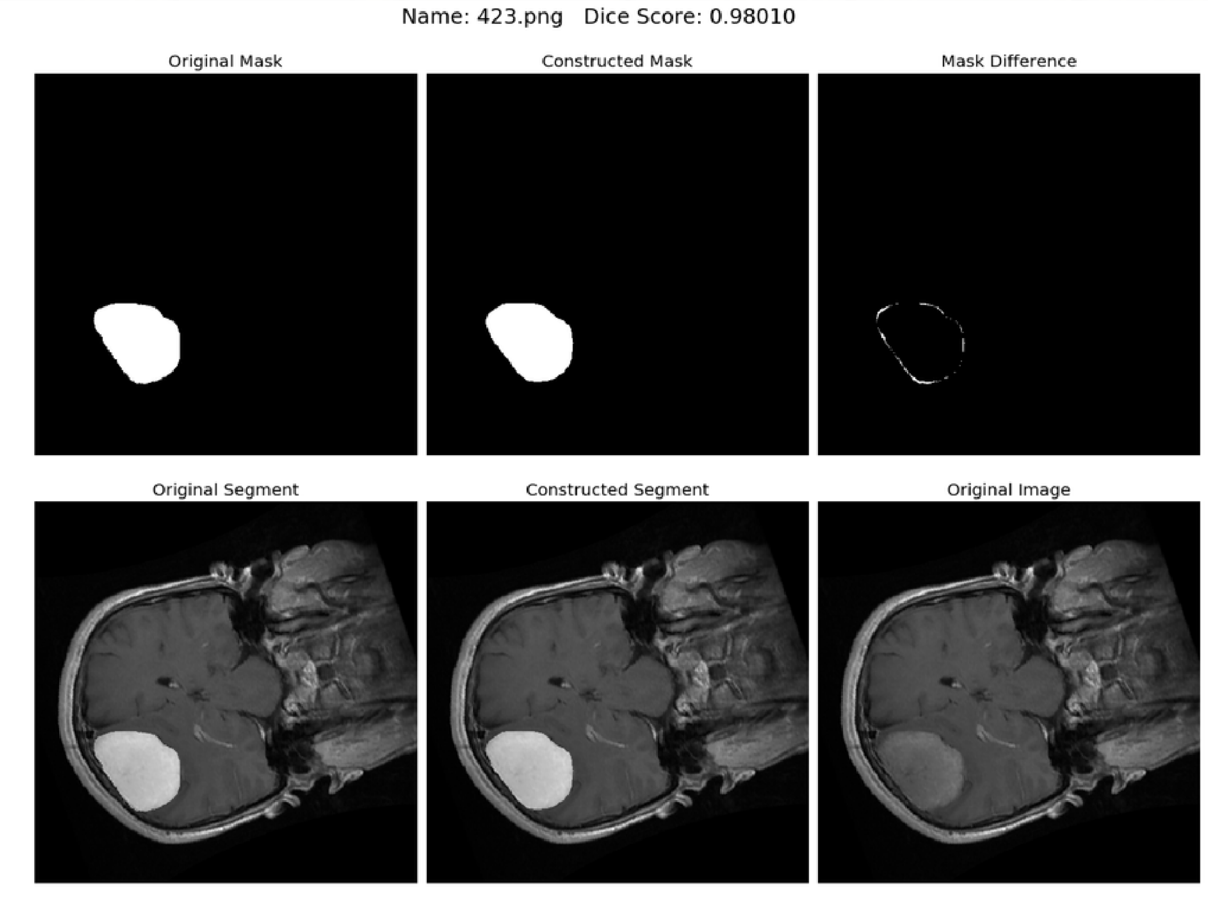
Training process

The model was trained on a Nvidia GTX 1050Ti 4GB GPU. Total time taken for model training was 6 hours and 45 minutes. We started with an initial learning rate of 1e-3 and reduced it by 85% on plateauing, final learning rate at the end of 100 epochs was 2.7249e-4.
Some graphs indicating Learning Rate & Loss Value over 100 epochs are given below.

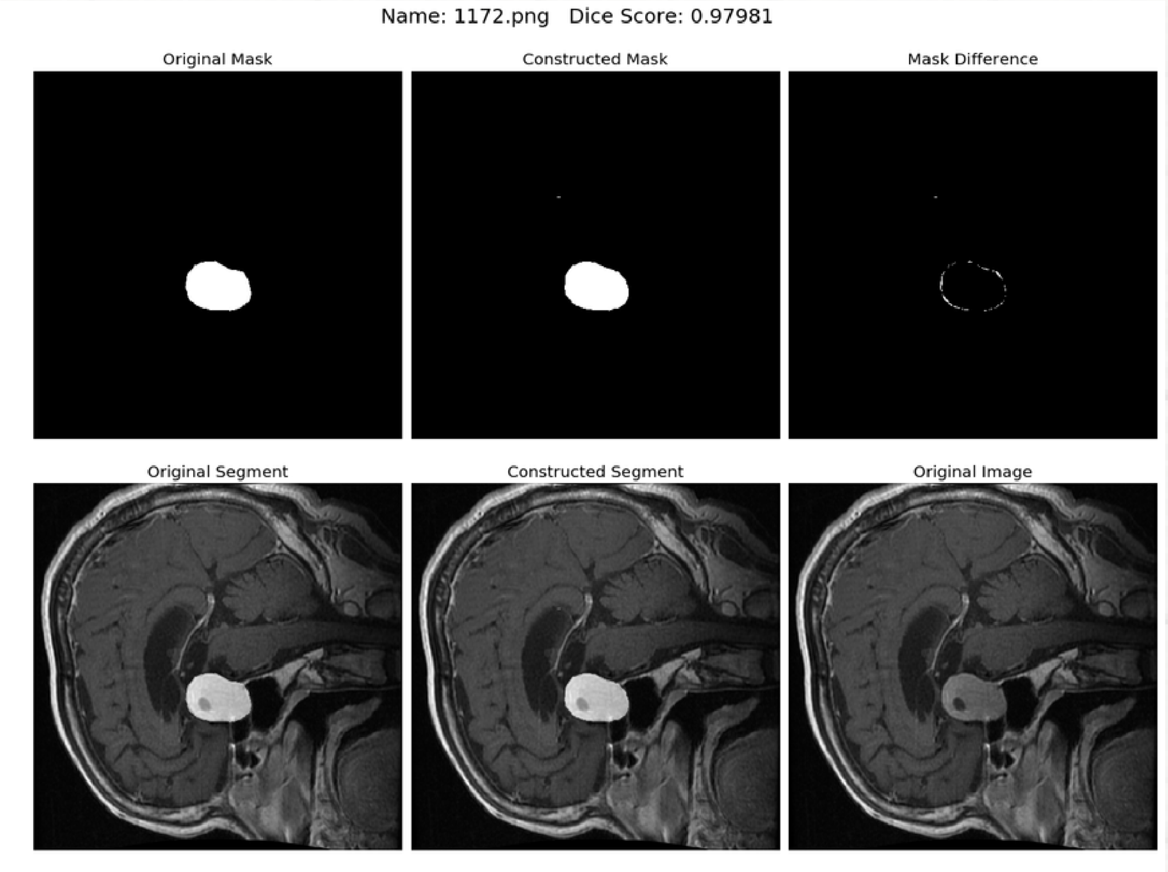




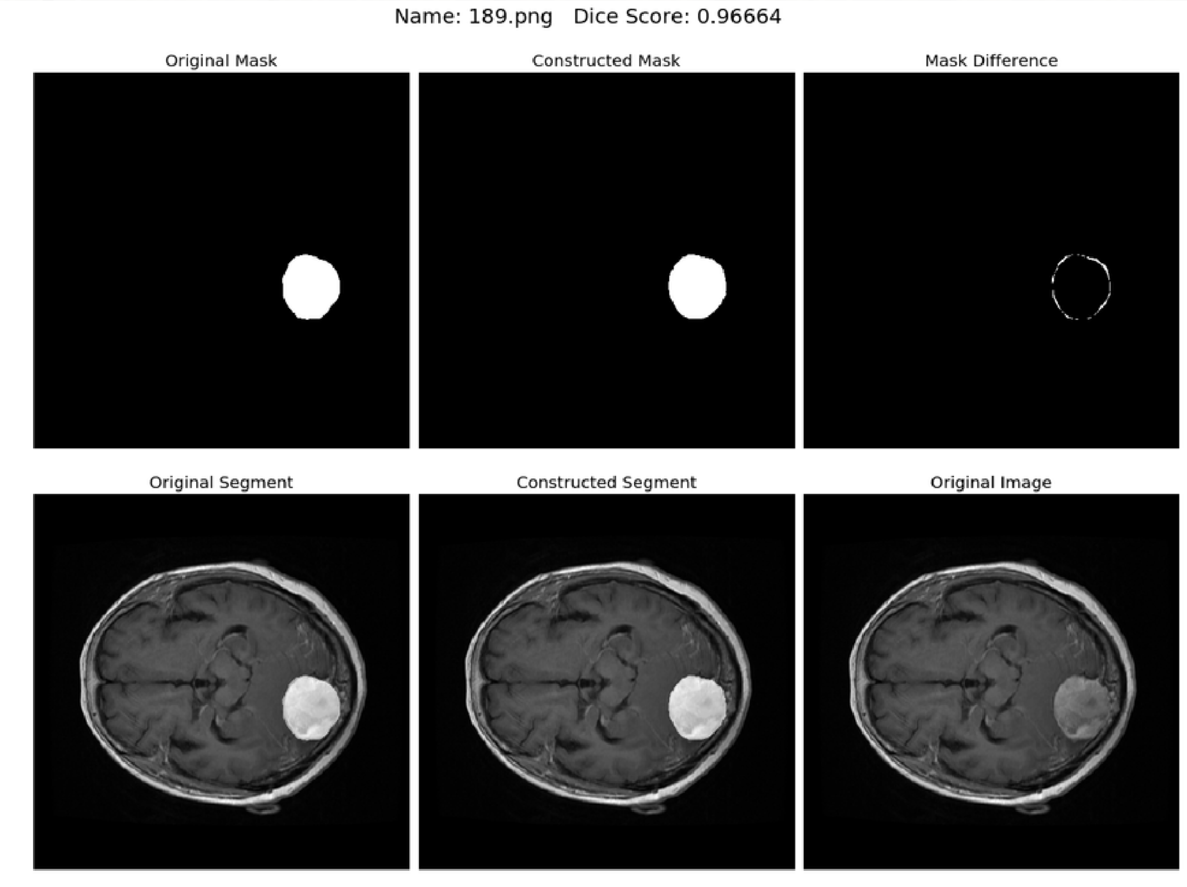
Results



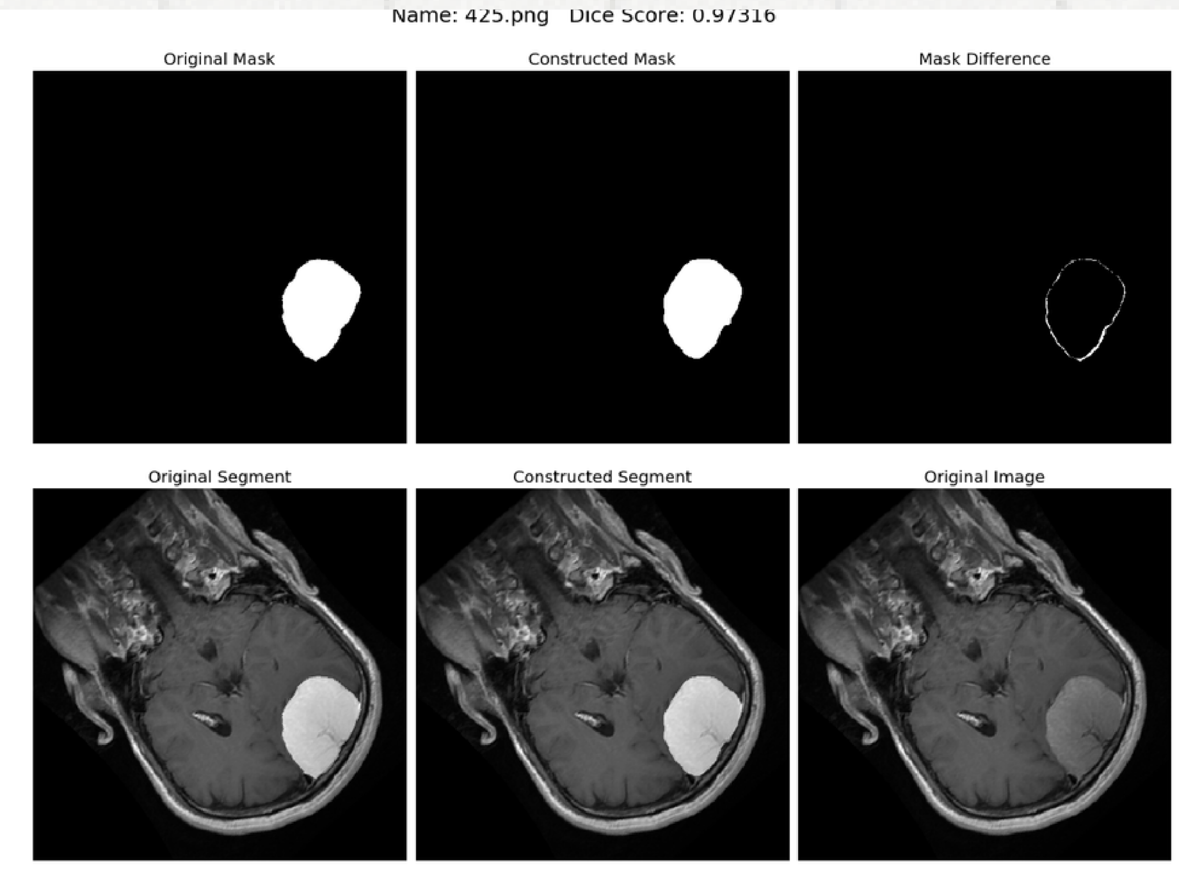
Name: 423.png Dice Score: 0.98010
Original Mask
Constructed Mask
Mask Difference
Original Segment
Constructed Segment
Original Image



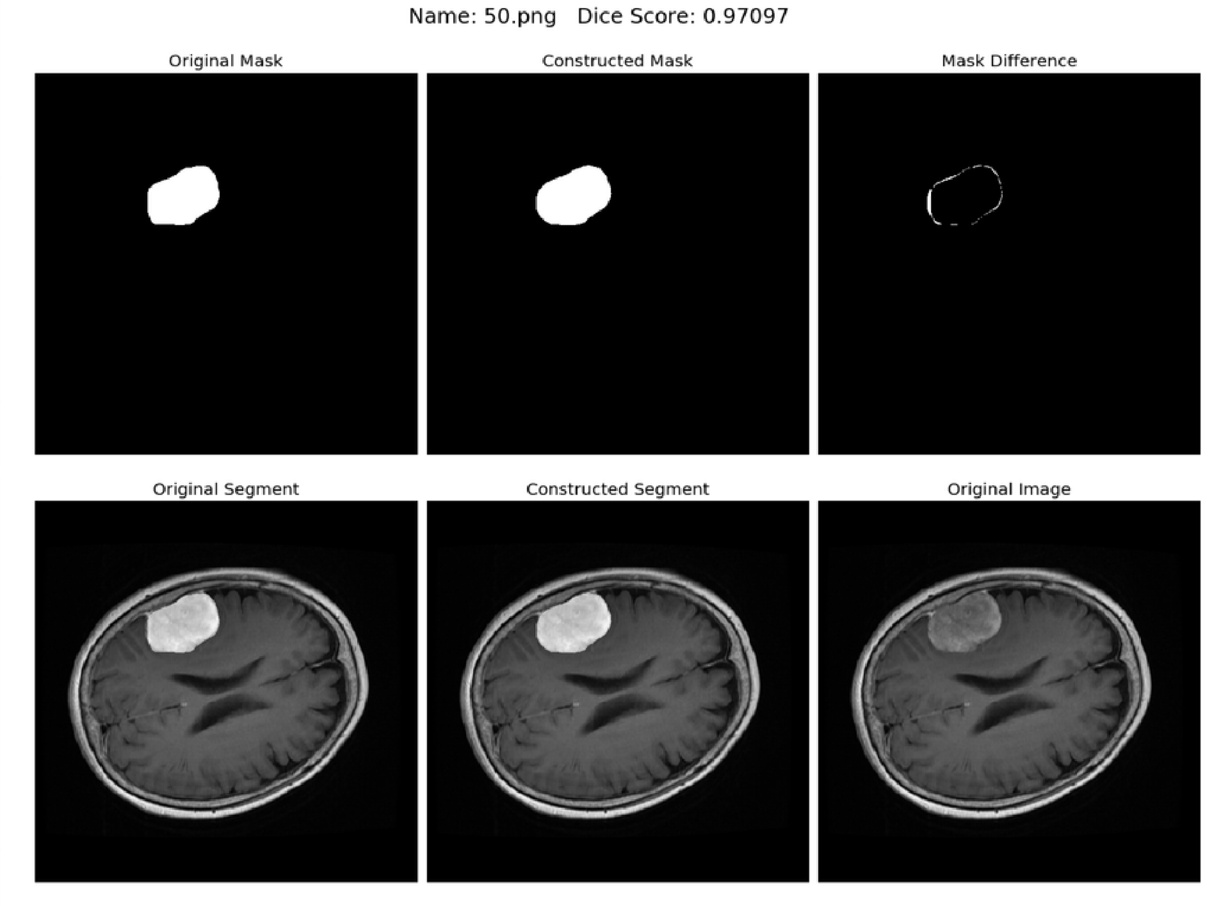
Name: 1172.png Dice Score: 0.97981
Original Mask
Constructed Mask
Mask Difference
Original Segment
Constructed Segment
Original Image



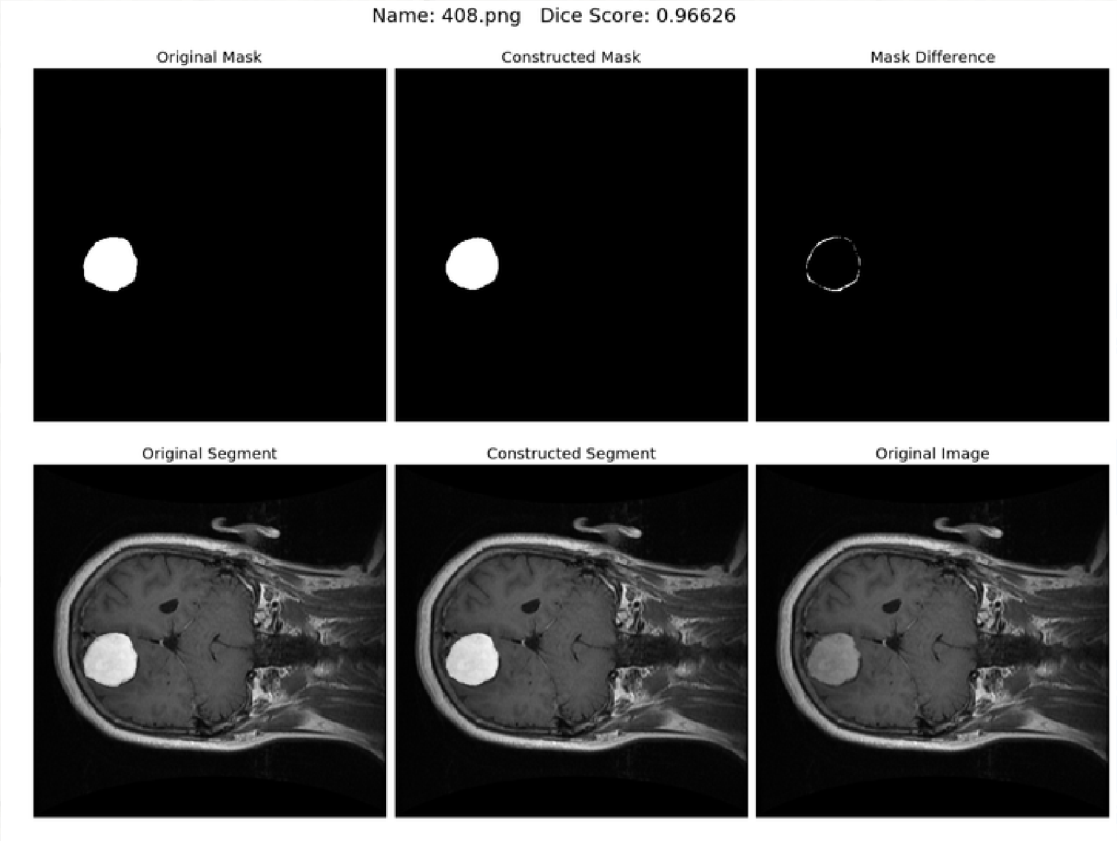
Name: 189.png Dice Score: 0.96664
Original Mask
Constructed Mask
Mask Difference
Original Segment
Constructed Segment
Original Image



Name: 425.png Dice Score: 0.97316
Original Mask
Constructed Mask
Mask Difference
Original Segment
Constructed Segment
Original Image



Name: 50.png Dice Score: 0.97097
Original Mask
Constructed Mask
Mask Difference
Original Segment
Constructed Segment
Original Image



Name: 408.png Dice Score: 0.96626
Original Mask
Constructed Mask
Mask Difference
Original Segment
Constructed Segment
Original Image

Conclusion

In conclusion, brain tumor segmentation is a crucial task in medical image analysis, with significant implications for patient diagnosis and treatment planning. Throughout this project, we have explored various aspects of brain tumor segmentation, including data augmentation, model architecture, and training strategies.

The model architecture for brain tumor segmentation typically involves a combination of convolutional neural network (CNN) components, including feature extraction backbones, contextual refinement modules, and multi-scale fusion techniques. These components work together to extract meaningful features from the input MRI volumes and generate accurate segmentation masks.

During the training process, we optimize our model parameters using annotated MRI volumes and corresponding tumor masks, leveraging loss functions tailored to handle class imbalance and encourage precise boundary delineation. Through iterative optimization and fine-tuning, our model learns to accurately segment brain tumor regions and produce clinically relevant results.

Thank you very much!